780

## SEQUENCE LISTING

<110> Luo, Ying Mancebo, Halena <120> NOVEL SYK KINASE-ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS, AND METHODS OF USE <130> A-68412-1/RMS/DHR <140> US 10/088,960 <141> 2002-03-22 <150> US 09/404,967 <151> 1999-09-24 <150> PCT/US 00/26338 <151> 2000-09-25 <160> 12 <170> PatentIn version 3.1 <210> 1 <211> 3955 <212> DNA <213> Homo sapiens <220> <221> misc\_feature <222> (1473)..(1473) <223> "n" at position 1473 can be any base. <400> 1 cggcagcaaa ggaacgtgcg aacgcgtgac gccgcccgac tggctcgcgc tetcccgtgc 60 eccagagtee teagecaget catagecaga gacagagag acaagagagag atgagagagag 120 180 cegegtggag acgtgaggeg geegeegtgg ceetcacagt eggegttteg eegeetgeee geggtgeeeg egeacgeetg cegecatege ettegegeet ggetggeggg ggegetgtee 240 teccaggeeg tecgegeege tecetggage teggeggage geggeageea gggeeggegg 300 aggegegagg ageegggege caeegeegee geegeegeeg eegeegeggg ggeeatgaee 360 gtggagcaga acgtgctgca gcagagcgcg gcgcagaagc accagcagac gtttttgaat 420 caactgagag aaattacggg gattaatgac acccagatac tacagcaagc cttgaaggat 480 agtaatggaa acttggaatt agoagtggct ttccttactg cgaagaatgc taagacccct 540 cagcaggagg agacaactta ctaccaaaca gcacttootg gcaatgatag atacatcagt 600 gtgggaagee aageagatae aaatgtgatt gateteactg gagatgataa agatgatett 660 cagagaacaa ttgccttgag tttggccgaa tcaaacaggg cattcaggga gactggaata 720

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10

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- Leu Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln 55
- Glu Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr
- Ile Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Cly
- Asp Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu
- Ser Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala 115 120
- Ile Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu
- Lys Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp
- Arg Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn 170 165
- Thr Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu 185
- Phe Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp 200
- Leu Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu 210
- Leu Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val 235
- Asp Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn 245 250

- Asp Ser Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp
- Trp Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu 280
- Glu Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu 290 295
- Ala Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe
- Gly Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys
- Leu Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu 345
- Asn Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro 360 355
- Val Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly 370
- Arg Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr
- Leu Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg 405 410
- Glu Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg
- Leu Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu 435 440
- Val Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val 450
- Cys Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly 465 470 475
- Ser Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala 490 485

- Leu Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile 500 505 510
- Ser Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro 515 520 525
- Pro Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu 530 535 540
- Leu Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu 545 550 555
- Asn Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr 565 570 575
- Ile Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg 580 585 590
- Leu His Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr 595 600 605
- Trp Ala Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn 610 615 620
- Asp Ile Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser 625 630 635 640
- Phe Gly Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn 645 650 655
- Asp Lys Ala Gln Phe Leu Ile Gln Glu Glu Phe Asn Lys Glu Thr Gly 660 665 670
- Gln Pro Leu Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe 675 680 685
- Val Glu Glu Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Glu Trp Asp 690 695 700
- Ala Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln 705 710 715 720
- Lys Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly
  725 730 735

- Asp Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His 740 745
- Leu Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His 760
- Glu Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu
- Tyr Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Fro Glu Thr 795
- Asp Tyr Arg Leu His His Val Val Tyr Phe Ile Gln Asn Gln Ala
- Pro Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg 825 820 830
- Asn Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln 840
- Ala Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr 855
- Glu Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr 875
- Leu Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser
- Leu Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser 905
- Lys Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg 915 920
- Arg Glu Cys Leu Leu Lys Leu Asn Glu Gln Ala Ala Glu Leu Phe Glu 930 935 940
- Ser Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile Ile Met Asn Glu 945 950
- Phe Ile Val Pro Phe Leu Pro Leu Leu Val Asp Glu Met Glu Glu 965

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                          1015
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Gly Arg
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